Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (original) In a computer system, a method of sequencing a nucleic acid sequence, the method comprising the steps of:

inputting hybridization intensities for a plurality of nucleic acid probes, the nucleic acid probes hybridizing with the nucleic acid sequence under conditions that do not allow identification of all of nucleic acid probes that are perfectly complementary to part of the nucleic acid sequence; and

sequencing the nucleic acid sequence according to selected nucleic acid probes.

2. (original) The method of claim 1, further comprising the step of selecting nucleic acid probes utilizing mismatch information among the nucleic acid probes.

3. (canceled)

4. (canceled)

5. (withdrawn) The method of claim 1, further comprising the step of selecting nucleic acid probes with highest hybridization intensities.

6. (withdrawn) The method of claim 5, wherein the nucleic acid probes with the highest hybridization intensities are above an intensity threshold.

7. (original) The method of claim 1, wherein the sequencing step includes the steps of:

aligning the selected nucleic acid probes so that bases that are common overlap; and

sequencing the nucleic acid sequence according to bases that occur most often at each position in the aligned nucleic acid probes.

8. (original) The method of claim 7, wherein the nucleic acid sequence is sequenced as complementary to the bases that occur most often.

9. (original) A computer program product that sequences a nucleic acid sequence, comprising:

computer readable code that receives as input hybridization intensities for a plurality of nucleic acid probes, the nucleic acid probes hybridizing with the nucleic acid sequence under conditions that do not allow identification of all nucleic acid probes that are perfectly complementary to part of the nucleic acid sequence; and

computer readable code that sequences the nucleic acid sequence according to selected nucleic acid probes;

wherein the computer readable codes are stored on a tangible medium.

Claims 10-26 (canceled)

27. (original) A method of sequencing a nucleic acid, comprising the steps of:

contacting a set of oligonucleotide probes of predetermined sequence and length with the nucleic acid under hybridization conditions that do not allow differentiation between (i) those probes of the set which are perfectly complementary to part of the nucleic acid and (ii) those probes that are not perfectly complementary to part of the nucleic acid;

selecting a subset of oligonucleotide probes that includes probes that are perfectly complementary to part of the nucleic acid and probes that are not perfectly complementary to part of the nucleic acid; and

determining the sequence of the nucleic acid by compiling overlapping sequences of the subset of probes.

28. (original) The method of claim 27, further comprising the step of fragmenting the nucleic acid before contacting the nucleic acid with the set of oligonucleotide probes.

29. (original) The method of claim 28, further comprising the step of labeling the nucleic acid before contacting the nucleic acid with the set of oligonucleotide probes.